How can metagenomics be used to address questions in ecology?

Jay T. Lennon

Indiana University

Metagenomics is a tool

The effect of a tool-driven revolution is to discover new things that have to be explained.

– Sir Frank Dyson, astronomer

The effect of a tool-driven revolution is to discover new things that have to be explained.

The effect of a concept-driven revolution is to explain old things in new ways.

– Sir Frank Dyson, astronomer

1) Metagenomics can be useful for description and discovery

Metagenomics lets us know “who is there”

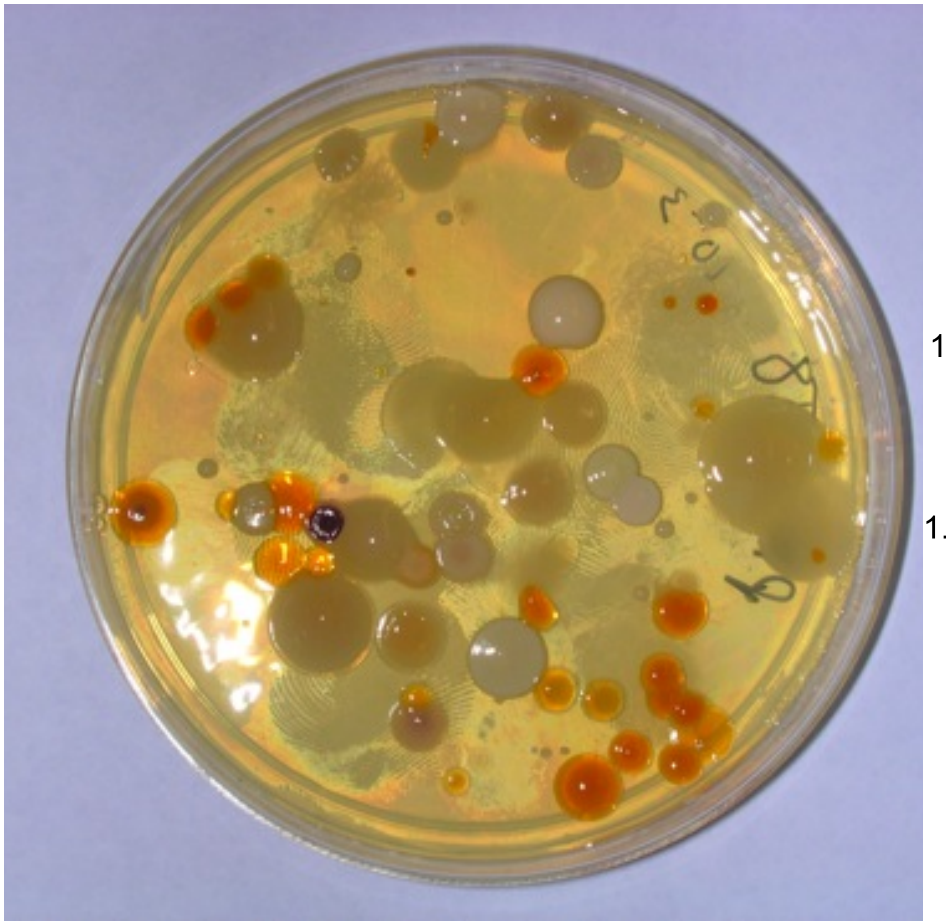
<u>Natural History</u>:

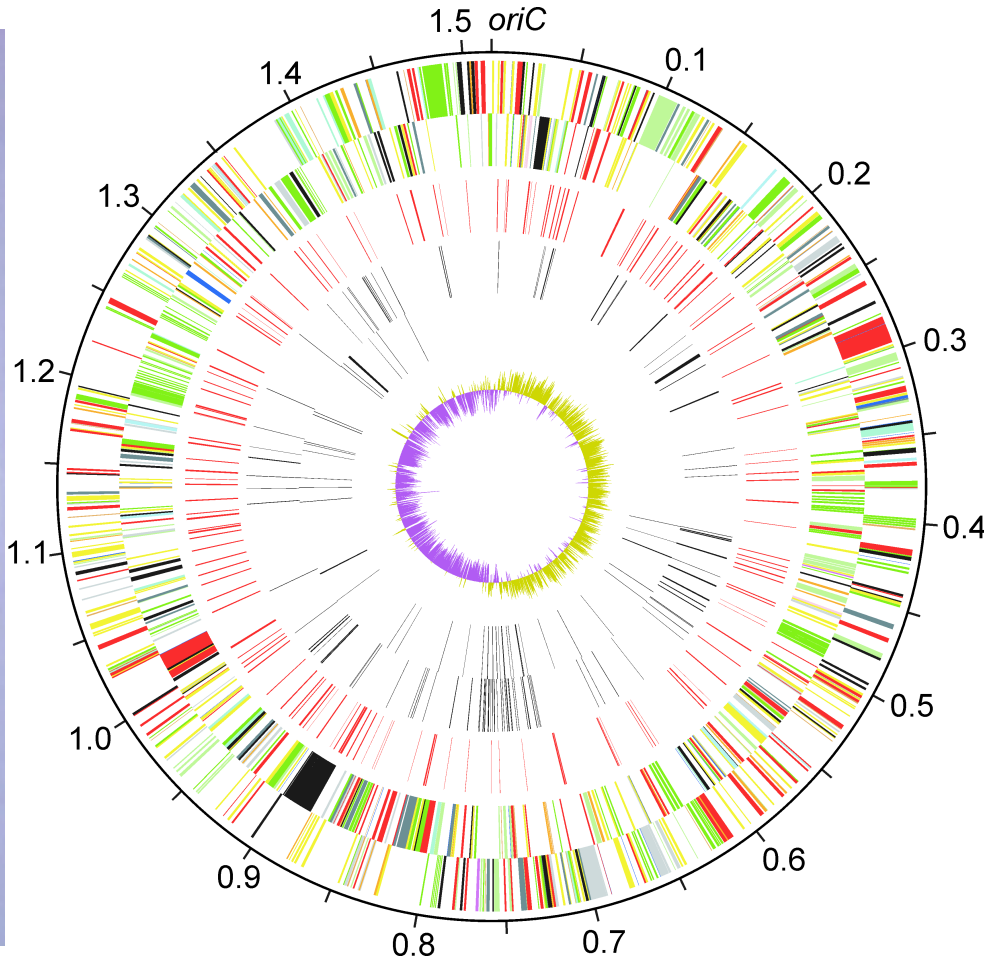
-Cataloging

-Exploration

-Inventory

Metagenomics may let us assemble (some) genomes without cultivation





Metagenomics lets us construct a “parts list”

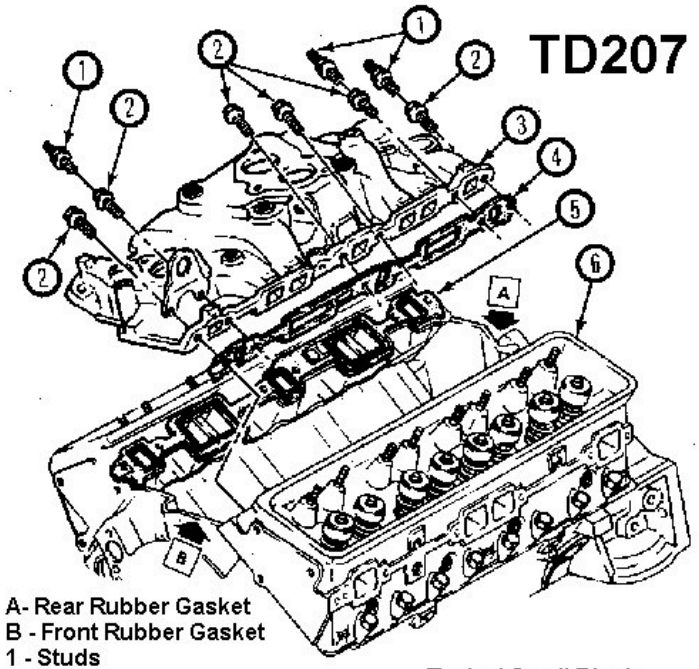
<u>Systems Biology</u>:

-What are the parts?

-Novel genes

-“Bioprospecting”

Metagenomics lets us “connect the parts”



Systems Biology:

-How do parts come together?

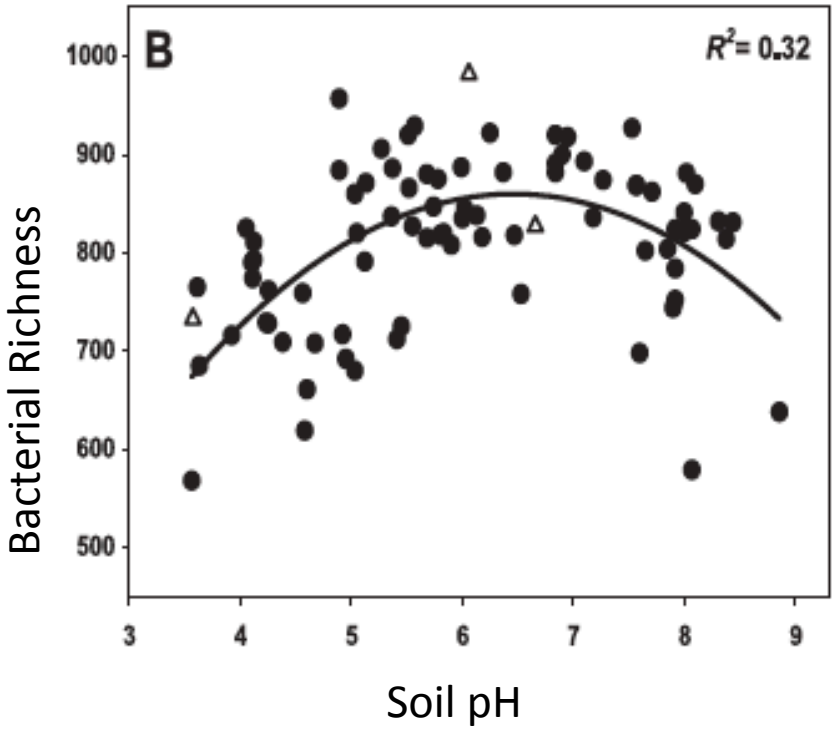
-Identify components

-Build up from bottom

2) Metagenomics can be useful for identifying patterns

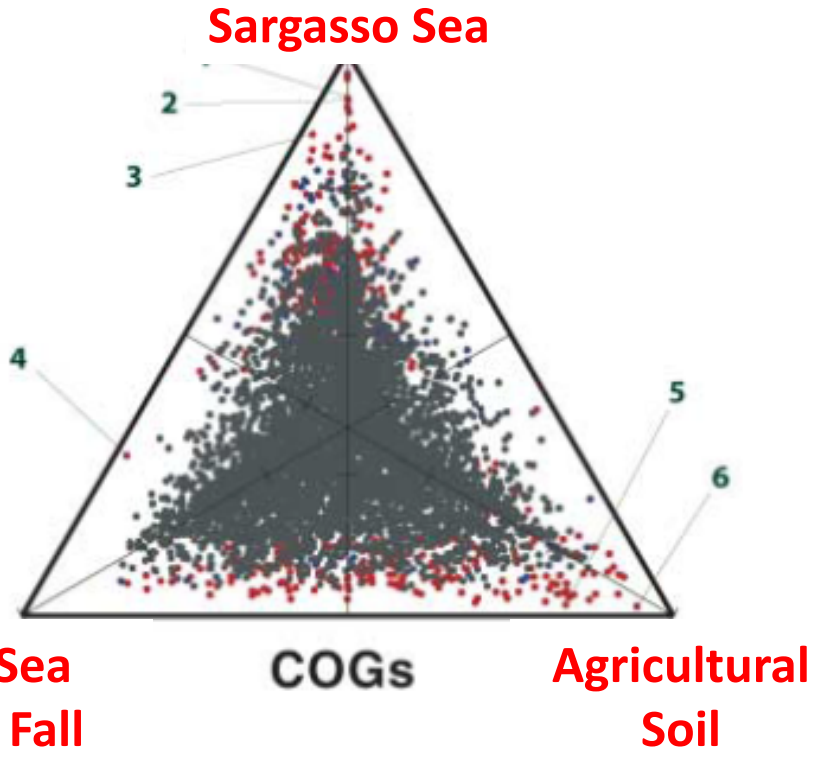
Metagenomics can identify new patterns

example of "targeted" metagenomics:



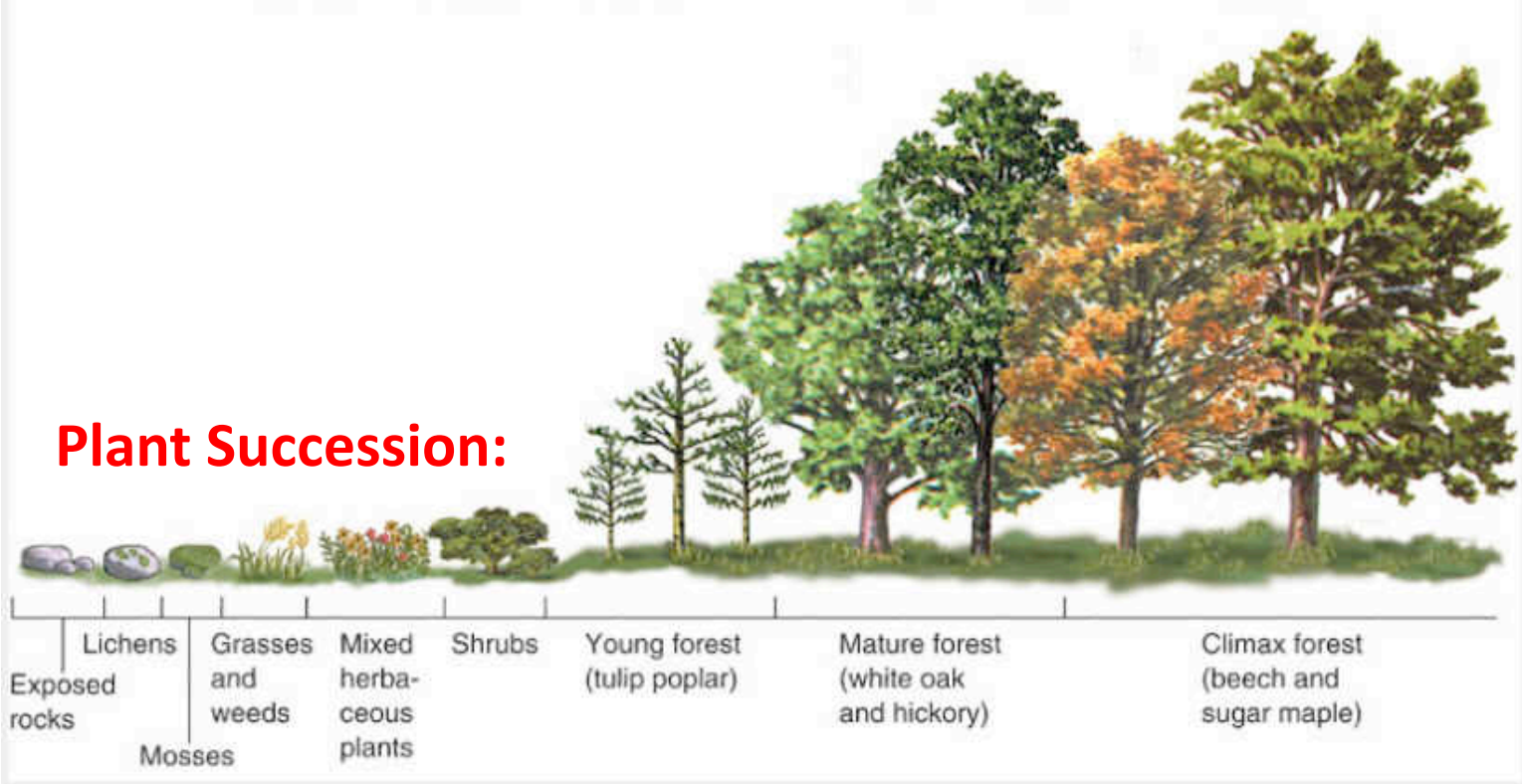
Lauber et al. (2009)

example of "shotgun" metagenomics:



Tringe et al. (2005)

Metagenomics can test for "old" patterns



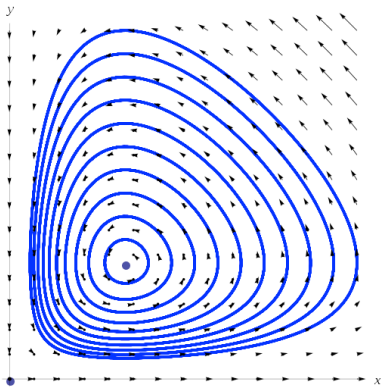
Do microbes obey same rules as "macrobes"?

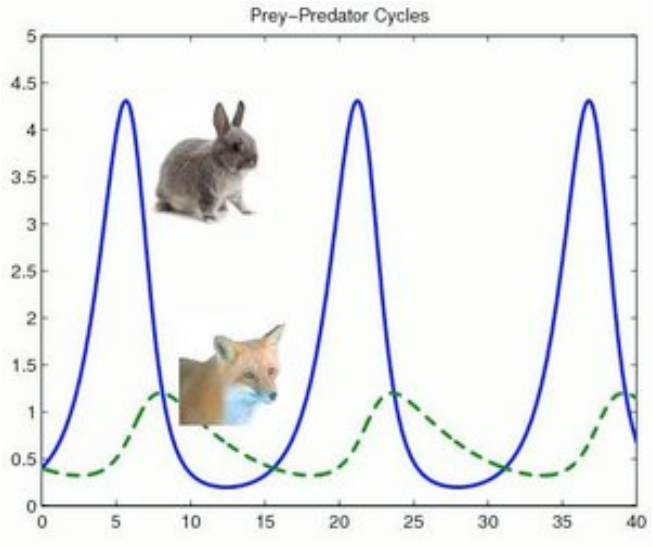
3) Can metagenomics be useful for prediction?

Relatively simple models in biology

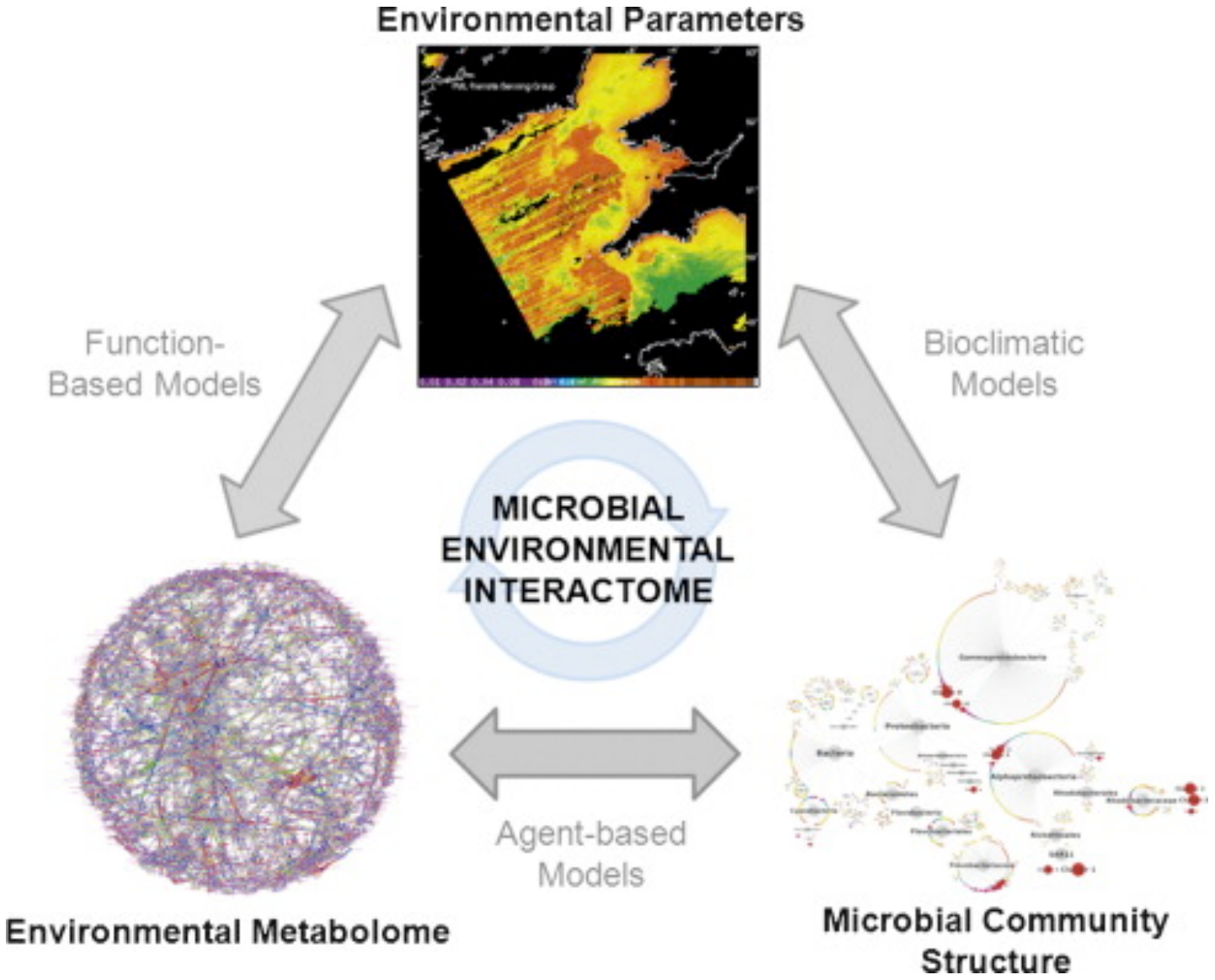
$$\frac{dN_1}{dt} = r_1 N_1 \left(\frac{K_1 - a_{11}N_1 - a_{12}N_2}{K_1} \right)$$

$$\frac{dN_2}{dt} = r_2 N_2 \left(\frac{K_2 - a_{21}N_1 - a_{22}N_2}{K_2} \right)$$





Relatively complex models



Larsen et al. 2012

“The ability to reduce everything to simple fundamental laws does not imply the ability to start from those laws and reconstruct the universe.”

– Phillip Warren Anderson, physicist

REVIEW

Mining the Biodiversity of Plants: A Revolution in the Making

Vincenzo De Luca,* Vonny Salim, Sayaka Masada Atsumi, Fang Yu

Only a small fraction of the immense diversity of plant metabolism has been explored for the production of new medicines and other products important to human well-being. The availability of inexpensive high-throughput sequencing is rapidly expanding the number of species that can be investigated for the speedy discovery of previously unknown enzymes and pathways.